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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=10; day=30; hr=14; min=31; sec=9; ms=215; ]

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Application No: 10578781

Version No: 1.0

Input Set:

Output Set:

Started: 2008-10-30 13:51:54.292

Finished: 2008-10-30 13:51:56.511

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 219 ms

Total Warnings: 35

Total Errors: 0

No. of SeqIDs Defined: 41

Actual SeqID Count: 41

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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W 213	Artificial or Unknown found in <213> in SEQ ID (12)
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W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)

**Input Set:**

**Output Set:**

**Started:** 2008-10-30 13:51:54.292  
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**No. of SeqIDs Defined:** 41  
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Error code

Error Description

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<110> HANAGATA, HIROSHI  
NISHIJYO, TAKAYUKI

<120> NOVEL BREVIBACILLUS CHOSHINENSIS AND METHOD FOR  
PRODUCING PROTEIN USING THE MICROORGANISM AS HOST

<130> 288727US-10578781

<140> 10578781

<141> 2008-10-30

<150> PCT/JP04/16912

<151> 2004-11-08

<150> JP 2003-381606

<151> 2003-11-11

<160> 41

<170> PatentIn Ver. 3.3

<210> 1

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<212> DNA

<213> Brevibacillus choshinensis

<220>

<221> CDS

<222> (1)..(753)

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Arg Glu Leu Leu Val Asn Ser Asn Ile Arg Leu Val Trp Ser Val Val	
35 40 45	

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ggg tgc att ggc ttg ctc aag gcc gtt gac aag ttc gat ctt tcg tac	240
Gly Cys Ile Gly Leu Leu Lys Ala Val Asp Lys Phe Asp Leu Ser Tyr	
65 70 75 80	

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Asp Val Arg Phe Ser Thr Tyr Ala Val Pro Met Ile Ile Gly Glu Ile	
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Lys Glu Thr Ala Asn Lys Val Arg Arg Ser Lys Asp Glu Leu Tyr Lys	
115 120 125	

caa ttc ggc cgt gcc ccc acg atc gca gaa gtg gca gaa gca gtg gga	432
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130 135 140	

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Ile Thr Pro Glu Glu Val Val Phe Ala Gln Glu Ala Ser Arg Ala Pro	
145 150 155 160	

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Ser Ser Ile His Glu Thr Val Phe Glu Asn Asp Gly Asp Pro Ile Thr	
165 170 175	

ctg atc gat cag ata gcg gat gaa ggt gtg aac aag tgg ttt gag aaa	576
Leu Ile Asp Gln Ile Ala Asp Glu Gly Val Asn Lys Trp Phe Glu Lys	
180 185 190	

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<211> 251

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<213> Brevibacillus choshinensis

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35 40 45

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 65 70 75 80  
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 85 90 95  
 Gln Arg Phe Leu Arg Asp Asp Gly Thr Val Lys Val Ser Arg Ser Leu  
 100 105 110  
 Lys Glu Thr Ala Asn Lys Val Arg Arg Ser Lys Asp Glu Leu Tyr Lys  
 115 120 125  
 Gln Phe Gly Arg Ala Pro Thr Ile Ala Glu Val Ala Glu Ala Val Gly  
 130 135 140  
 Ile Thr Pro Glu Glu Val Val Phe Ala Gln Glu Ala Ser Arg Ala Pro  
 145 150 155 160  
 Ser Ser Ile His Glu Thr Val Phe Glu Asn Asp Gly Asp Pro Ile Thr  
 165 170 175  
 Leu Ile Asp Gln Ile Ala Asp Glu Gly Val Asn Lys Trp Phe Glu Lys  
 180 185 190  
 Ile Ala Leu Lys Asp Ala Ile Ser Arg Leu Ser Glu Arg Glu Gln Leu  
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<212> DNA

<213> Brevibacillus choshinensis

<220>

<221> CDS

<222> (1)..(2262)

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 tcc tca ctg gtc ctg agc ggc att gcg gcg gtt cca gcg aca ggg atg 96  
 Ser Ser Leu Val Leu Ser Gly Ile Ala Ala Val Pro Ala Thr Gly Met

20										25										30										
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Ala Lys Ser Lys Asp Lys Pro Pro Leu Glu Val Asp Leu Ser Thr Val																														
35 40 45																														
aac atg gat cgt ttg gtt aaa gcc ttg atc gac caa ggt gaa atc gac	192																													
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50 55 60																														
gag gac gcc gac cag gaa gag atc aac aaa gct gtg gag aag ttt ttg	240																													
Glu Asp Ala Asp Gln Glu Glu Ile Asn Lys Ala Val Glu Lys Phe Leu																														
65 70 75 80																														
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Arg Asp Lys Lys Val Pro His Gly Ile Asp Asp Ser Ser Ser Phe Gly																														
85 90 95																														
aaa aaa gca agc aaa acc cag ctt tcg gca gta tca aag gca gca agc	336																													
Lys Lys Ala Ser Lys Thr Gln Leu Ser Ala Val Ser Lys Ala Ala Ser																														
100 105 110																														
aaa gta tcc aag ctc aaa gat gac aag caa gtg cgc gct tcc aag cgg	384																													
Lys Val Ser Lys Leu Lys Asp Asp Lys Gln Val Arg Ala Ser Lys Arg																														
115 120 125																														
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Val His Thr Asp Asn Leu Val Ile Ala Leu Val Glu Phe Asn Asp Leu																														
130 135 140																														
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245 250 255																														

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Pro Tyr Asp Leu Asp Gly Asp Ser Asp Leu Met Glu Pro Asp Gly Met	
260 265 270	
ctg gac aac ctg atg ctg gtt cac tcc ggt att ggt gaa gag act ggg	864
Leu Asp Asn Leu Met Leu Val His Ser Gly Ile Gly Glu Glu Thr Gly	
275 280 285	
gaa gat gcg gat gcg atc tgg tct cac cgc tgg act ctg aaa aag ccg	912
Glu Asp Ala Asp Ala Ile Trp Ser His Arg Trp Thr Leu Lys Lys Pro	
290 295 300	
aca gaa att cca ggc acc agc ctg aaa gct tac gac tac atg att cag	960
Thr Glu Ile Pro Gly Thr Ser Leu Lys Ala Tyr Asp Tyr Met Ile Gln	
305 310 315 320	
cct gaa gat ggc gca ccc ggc gta ttc gca cat gaa tac gga cac aac	1008
Pro Glu Asp Gly Ala Pro Gly Val Phe Ala His Glu Tyr Gly His Asn	
325 330 335	
ctg gga ctg cca gat ctg tat gac acg aca aga ctg gga cat gat tcg	1056
Leu Gly Leu Pro Asp Leu Tyr Asp Thr Thr Arg Leu Gly His Asp Ser	
340 345 350	
ccg gtt ggc gca tgg tcg ctg atg tct tcc gga agc cat aca ggt aag	1104
Pro Val Gly Ala Trp Ser Leu Met Ser Ser Gly Ser His Thr Gly Lys	
355 360 365	
atc ttc caa acc caa cca acc gga ttt gat cct tgg tcc aaa atg atg	1152
Ile Phe Gln Thr Gln Pro Thr Gly Phe Asp Pro Trp Ser Lys Met Met	
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ctg cag gaa atg tat ggg ggc aag tgg att gag ccg caa gtc atc aat	1200
Leu Gln Glu Met Tyr Gly Gly Lys Trp Ile Glu Pro Gln Val Ile Asn	
385 390 395 400	
tac gaa gac ctg aaa aaa cgg aaa aag cag gct tcg ctc tac gat ggc	1248
Tyr Glu Asp Leu Lys Lys Arg Lys Lys Gln Ala Ser Leu Tyr Asp Gly	
405 410 415	
agc agc ctc gat gaa gat ggc aaa gtc atc aag ctg aat atg ccg caa	1296
Ser Ser Leu Asp Glu Asp Gly Lys Val Ile Lys Leu Asn Met Pro Gln	
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Val Glu Lys Thr Pro Pro Val Gln Pro Lys Asp Gly Asp Tyr Ser Tyr	
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Phe Ser Asp Glu Gly Asp Asn Leu Asn Thr Lys Met Thr Ser Glu Val	
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465 470 475 480	



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Arg Ala Ile Glu Thr Gly Tyr Asp Tyr Leu Tyr Val Asn Val Ile Asp	
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Val Asp Ser Gly Glu Ser Thr Thr Val Lys Glu Tyr Asp Asp Glu Thr	
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Lys Gly Trp Asp Lys Glu Glu Ile Ser Leu Asn Asp Phe Ala Gly Lys	
515 520 525	
aag att caa gtc gag ttc aac tac gtg acg gat ggc ggc ttg gcg atg	1632
Lys Ile Gln Val Glu Phe Asn Tyr Val Thr Asp Gly Gly Leu Ala Met	
530 535 540	
tcc ggc ttc tat ctg gat aat ttt gca gtc aca gca gac ggc gaa gta	1680
Ser Gly Phe Tyr Leu Asp Asn Phe Ala Val Thr Ala Asp Gly Glu Val	
545 550 555 560	
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Phe Ile His Phe Asp Gly Glu Gly Lys Met Tyr Asp Ala Tyr Tyr Leu	
580 585 590	
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Val Glu Leu Arg Ser His Glu Gly Val Asp Glu Gly Leu Lys Tyr Phe	
595 600 605	
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Arg Arg Asn Asp Thr Phe Phe Thr Tyr Asp Pro Gly Leu Val Ile Trp	
610 615 620	
tac tac gat gga cgc ttt ggc aaa acg caa gac aac aac acc agc aac	1920
Tyr Tyr Asp Gly Arg Phe Gly Lys Thr Gln Asp Asn Asn Thr Ser Asn	
625 630 635 640	
cat cca ggc tac ggc atg ctg ggc gta gtc gat gcg cat cag gaa gtt	1968
His Pro Gly Tyr Gly Met Leu Gly Val Val Asp Ala His Gln Glu Val	
645 650 655	
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660 665 670	
cgt tac caa gtg aac gat gcg gca ttc agc ccg aac aaa acc tcc ggc	2064
Arg Tyr Gln Val Asn Asp Ala Ala Phe Ser Pro Asn Lys Thr Ser Gly	
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 725 730 735

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Glu Asp Ala Asp Gln Glu Glu Ile Asn Lys Ala Val Glu Lys Phe Leu  
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Arg Asp Lys Lys Val Pro His Gly Ile Asp Asp Ser Ser Ser Phe Gly  
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Lys Lys Ala Ser Lys Thr Gln Leu Ser Ala Val Ser Lys Ala Ala Ser  
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Glu His Asn Gln Val Pro Lys Gln Ser Asp Ser Leu Trp Thr Ala Asp  
 145 150 155 160

Phe Asp Gln Lys His Tyr Glu Glu Met Leu Phe Asp Arg Lys Gly Tyr  
 165 170 175

Thr Thr Pro Glu Gly Ile Ser Met Thr Thr Met Ala Lys Tyr Tyr Tyr  
 180 185 190

Glu Gln Ser Gly Glu Thr Trp Thr Val Asp Gly Val Val Thr Pro Trp  
195 200 205

Leu Thr Ala Glu Lys Asp Lys Lys Phe T